Refine Search

Search Results -

Terms	Documents
L2 and (pelz or dinman or czaplinski).in.	5

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Search: L3

Refine Search | Recall Text | Clear | Interrupt

Search History

DATE: Wednesday, July 28, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR			
L3	L2 and (pelz or dinman or czaplinski).in.	5	L3
L2	L1 and (upf$4 or nam7$4 or sal1$4 or ifs2$4 or mof4$4 or nmd2$4 or isf1$4 or sua1$4 or sua6$4)	40	L2
L1	(HELICAS$4 OR MTT1$4) AND (ERF$4 OR (RELEAS$4 same FACTO$4))	500	L1

END OF SEARCH HISTORY

Hit List

Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs | Generate OACS

Search Results - Record(s) 1 through 5 of 5 returned.

☐ 1. Document ID: US 20040115787 A1

Using default format because multiple data bases are involved.

L3: Entry 1 of 5 File: PGPB Jun 17, 2004

PGPUB-DOCUMENT-NUMBER: 20040115787
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040115787 A1

TITLE: Subfamily of RNA helicases which are modulators of the fidelity of translation termination and uses thereof

PUBLICATION-DATE: June 17, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Peltz, Stuart	Piscataway	NJ	US	
Czaplinski, Kevin	Somerset	NJ	US	
Dinman, Jonathan D.	North Brunswick	NJ	US	

US-CL-CURRENT: 435/226; 530/388.26, 536/23.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 2. Document ID: US 20030032158 A1

L3: Entry 2 of 5 File: PGPB Feb 13, 2003

PGPUB-DOCUMENT-NUMBER: 20030032158
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030032158 A1

TITLE: Method of modulating the efficiency of translation termination and degradation of aberrant mRNA involving a surveillance complex comprising human Upf1p,eucaryotic release factor 1 and eucaryotic release factor 3

PUBLICATION-DATE: February 13, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Peltz, Stuart	Piscataway	NJ	US	
Czaplinski, Kevin	Somerset	NJ	US	

Weng, Youmin Cranford NJ US

US-CL-CURRENT: 435/189; 530/388.26

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De

---

☐ 3. Document ID: US 6630294 B1

L3: Entry 3 of 5 File: USPT Oct 7, 2003

US-PAT-NO: 6630294
DOCUMENT-IDENTIFIER: US 6630294 B1

TITLE: Subfamily of RNA helicases which are modulators of the fidelity of translation termination and uses thereof

DATE-ISSUED: October 7, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Peltz; Stuart	Piscataway	NJ		
Czaplinski; Kevin	Somerset	NJ		
Dinman; Jonathan D.	North Brunswick	NJ		

US-CL-CURRENT: 435/4; 435/183, 435/7.1, 435/7.31, 436/86, 530/350, 536/23.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De

---

☐ 4. Document ID: US 6486305 B1

L3: Entry 4 of 5 File: USPT Nov 26, 2002

US-PAT-NO: 6486305
DOCUMENT-IDENTIFIER: US 6486305 B1

TITLE: METHOD OF MODULATING THE EFFICIENCY OF TRANSLATION TERMINATION AND DEGRADATION OF ABERRANT MRNA INVOLVING A SURVEILLANCE COMPLEX COMPRISING HUMAN UPF1P, EUCARYOTIC RELEASE FACTOR 1 AND EUCARYOTIC RELEASE FACTOR 3

DATE-ISSUED: November 26, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Peltz; Stuart	Piscataway	NJ	08854	
Czaplinski; Kevin	Somerset	NJ	08873	
Weng; Youmin	Cranford	NJ	07016	

US-CL-CURRENT: 530/412; 435/455, 435/69.1, 530/350, 530/358

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De

☐ 5. Document ID: US 20040115787 A1

L3: Entry 5 of 5 File: DWPI Jun 17, 2004

DERWENT-ACC-NO: 2004-449400
DERWENT-WEEK: 200442

TITLE: Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent inhibits the MTT1

INVENTOR: CZAPLINSKI, K; DINMAN, J D ; PELTZ, S

PRIORITY-DATA: 1998US-093685P (July 22, 1998), 1999US-0359268 (July 22, 1999), 2003US-0652334 (August 28, 2003)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 20040115787 A1	June 17, 2004		041	C12N009/64

INT-CL (IPC): C07 H 21/04; C07 K 16/40; C12 N 9/64

Terms	Documents
L2 and (pelz or dinman or czaplinski).in.	5

=> d his

(FILE 'HOME' ENTERED AT 19:31:12 ON 28 JUL 2004)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 19:31:26 ON 28 JUL 2004

SEA (HELICAS? OR MTT1?) OR (ERF? OR (RELEAS?(S)FACTO?))

1596 FILE ADISCTI
354 FILE ADISINSIGHT
378 FILE ADISNEWS
6851 FILE AGRICOLA
192 FILE ANABSTR
2954 FILE AQUASCI
1469 FILE BIOBUSINESS
234 FILE BIOCOMMERCE
43311 FILE BIOSIS
2564 FILE BIOTECHABS
2564 FILE BIOTECHDS
25707 FILE BIOTECHNO
14587 FILE CABA
22758 FILE CANCERLIT
50487 FILE CAPLUS
60171 FILE CEABA-VTB
83 FILE CEN
444 FILE CIN
1196 FILE CONFSCI
306 FILE CROPB
455 FILE CROPU
4438 FILE DISSABS
10295 FILE DDFB
18653 FILE DDFU
399612 FILE DGENE
10295 FILE DRUGB
41 FILE DRUGMONOG2
183 FILE IMSDRUGNEWS
21744 FILE DRUGU
192 FILE IMSRESEARCH
721 FILE EMBAL
83157 FILE EMBASE
27817 FILE ESBIOBASE
3955* FILE FEDRIP
304 FILE FOMAD
475 FILE FROSTI
1816 FILE FSTA
17804 FILE GENBANK
453 FILE HEALSAFE
3074 FILE IFIPAT
72 FILE IMSPRODUCT
4377 FILE JICST-EPLUS
246 FILE KOSMET
20977 FILE LIFESCI
76 FILE MEDICONF
59476 FILE MEDLINE
844 FILE NIOSHTIC
3489 FILE NTIS
11 FILE NUTRACEUT
754 FILE OCEAN
44363 FILE PASCAL
431 FILE PHAR
130 FILE PHARMAML
5 FILE PHIC
788 FILE PHIN
304170 FILE PROMT
1131 FILE PROUSDDR
475 FILE RDISCLOSURE
58511 FILE SCISEARCH
10 FILE SYNTHLINE

20905 FILE TOXCENTER
43056 FILE USPATFULL
2544 FILE USPAT2
829 FILE VETB
2402 FILE VETU
4638 FILE WPIDS
1925 FILE WPIFV
4638 FILE WPINDEX
944 FILE IPA
171 FILE NAPRALERT
19988 FILE NLDB

L1 QUE (HELICAS? OR MTT1?) OR (ERF? OR (RELEAS?(S) FACTO?))

FILE 'DGENE, PROMT, EMBASE, CEABA-VTB, MEDLINE, SCISEARCH, CAPLUS, PASCAL, BIOSIS, USPATFULL, ESBIOBASE' ENTERED AT 19:35:08 ON 28 JUL 2004

L2 673 S (HELICAS? OR MTT1?) AND (ERF? OR (RELEAS?(S)FACTO?))
L3 51 S L2 AND (UPF? OR NAM7? OR SAL1? OR IFS2? OR MOF4? OR NMD2? OR
L4 46 DUP REM L3 (5 DUPLICATES REMOVED)

```
Welcome to STN International!  Enter x:x

LOGINID:ssspta1652dmr

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2          "Ask CAS" for self-help around the clock
 NEWS  3  May 12  EXTEND option available in structure searching
 NEWS  4  May 12  Polymer links for the POLYLINK command completed in REGISTRY
 NEWS  5  May 27  New UPM (Update Code Maximum) field for more efficient patent
                  SDIs in CAplus
 NEWS  6  May 27  CAplus super roles and document types searchable in REGISTRY
 NEWS  7  Jun 28  Additional enzyme-catalyzed reactions added to CASREACT
 NEWS  8  Jun 28  ANTE, AQUALINE, BIOENG, CIVILENG, ENVIROENG, MECHENG,
                  and WATER from CSA now available on STN(R)
 NEWS  9  Jul 12  BEILSTEIN enhanced with new display and select options,
                  resulting in a closer connection to BABS

 NEWS EXPRESS  MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT
               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN Customer
  agreement.  Please note that this agreement limits use to scientific
  research.  Use for software development or design or implementation
  of commercial gateways or other similar uses is prohibited and may
  result in loss of user privileges and other penalties.

  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 19:31:12 ON 28 JUL 2004

=> index bioscience medicine
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,
       BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
       CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU,
       DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 19:31:26 ON 28 JUL 2004

73 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s (helicas? or mtt1?) or (erf? or (releas?(s)facto?))
       1596   FILE ADISCTI
        354   FILE ADISINSIGHT
        378   FILE ADISNEWS
       6851   FILE AGRICOLA
        192   FILE ANABSTR
       2954   FILE AQUASCI
```

```
      1469   FILE BIOBUSINESS
       234   FILE BIOCOMMERCE
     43311   FILE BIOSIS
      2564   FILE BIOTECHABS
      2564   FILE BIOTECHDS
     25707   FILE BIOTECHNO
     14587   FILE CABA
     22758   FILE CANCERLIT
     50487   FILE CAPLUS
     60171   FILE CEABA-VTB
        83   FILE CEN
       444   FILE CIN
      1196   FILE CONFSCI
       306   FILE CROPB
       455   FILE CROPU
21 FILES SEARCHED...
      4438   FILE DISSABS
     10295   FILE DDFB
     18653   FILE DDFU
    399612   FILE DGENE
     10295   FILE DRUGB
        41   FILE DRUGMONOG2
       183   FILE IMSDRUGNEWS
     21744   FILE DRUGU
       192   FILE IMSRESEARCH
       721   FILE EMBAL
     83157   FILE EMBASE
     27817   FILE ESBIOBASE
      3955*  FILE FEDRIP
       304   FILE FOMAD
35 FILES SEARCHED...
       475   FILE FROSTI
      1816   FILE FSTA
     17804   FILE GENBANK
       453   FILE HEALSAFE
      3074   FILE IFIPAT
        72   FILE IMSPRODUCT
      4377   FILE JICST-EPLUS
       246   FILE KOSMET
     20977   FILE LIFESCI
        76   FILE MEDICONF
     59476   FILE MEDLINE
       844   FILE NIOSHTIC
      3489   FILE NTIS
        11   FILE NUTRACEUT
       754   FILE OCEAN
     44363   FILE PASCAL
       431   FILE PHAR
       130   FILE PHARMAML
         5   FILE PHIC
       788   FILE PHIN
57 FILES SEARCHED...
    304170   FILE PROMT
      1131   FILE PROUSDDR
       475   FILE RDISCLOSURE
     58511   FILE SCISEARCH
        10   FILE SYNTHLINE
     20905   FILE TOXCENTER
     43056   FILE USPATFULL
      2544   FILE USPAT2
       829   FILE VETB
      2402   FILE VETU
      4638   FILE WPIDS
      1925   FILE WPIFV
      4638   FILE WPINDEX
       944   FILE IPA
       171   FILE NAPRALERT
     19988   FILE NLDB

71 FILES HAVE ONE OR MORE ANSWERS,   73 FILES SEARCHED IN STNINDEX
```

L1 QUE (HELICAS? OR MTT1?) OR (ERF? OR (RELEAS?(S) FACTO?))

=> d rank

F1	399612	DGENE
F2	304170	PROMT
F3	83157	EMBASE
F4	60171	CEABA-VTB
F5	59476	MEDLINE
F6	58511	SCISEARCH
F7	50487	CAPLUS
F8	44363	PASCAL
F9	43311	BIOSIS
F10	43056	USPATFULL
F11	27817	ESBIOBASE
F12	25707	BIOTECHNO
F13	22758	CANCERLIT
F14	21744	DRUGU
F15	20977	LIFESCI
F16	20905	TOXCENTER
F17	19988	NLDB
F18	18653	DDFU
F19	17804	GENBANK
F20	14587	CABA
F21	10295	DDFB
F22	10295	DRUGB
F23	6851	AGRICOLA
F24	4638	WPIDS
F25	4638	WPINDEX
F26	4438	DISSABS
F27	4377	JICST-EPLUS
F28	3955*	FEDRIP
F29	3489	NTIS
F30	3074	IFIPAT
F31	2954	AQUASCI
F32	2564	BIOTECHABS
F33	2564	BIOTECHDS
F34	2544	USPAT2
F35	2402	VETU
F36	1925	WPIFV
F37	1816	FSTA
F38	1596	ADISCTI
F39	1469	BIOBUSINESS
F40	1196	CONFSCI
F41	1131	PROUSDDR
F42	944	IPA
F43	844	NIOSHTIC
F44	829	VETB
F45	788	PHIN
F46	754	OCEAN
F47	721	EMBAL
F48	475	FROSTI
F49	475	RDISCLOSURE
F50	455	CROPU
F51	453	HEALSAFE
F52	444	CIN
F53	431	PHAR
F54	378	ADISNEWS
F55	354	ADISINSIGHT
F56	306	CROPB
F57	304	FOMAD
F58	246	KOSMET
F59	234	BIOCOMMERCE
F60	192	ANABSTR
F61	192	IMSRESEARCH
F62	183	IMSDRUGNEWS
F63	171	NAPRALERT
F64	130	PHARMAML
F65	83	CEN
F66	76	MEDICONF
F67	72	IMSPRODUCT
F68	41	DRUGMONOG2

```
F69          11   NUTRACEUT
F70          10   SYNTHLINE
F71           5   PHIC


=> file f1-f11
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     3.42       3.63

FILE 'DGENE' ENTERED AT 19:35:08 ON 28 JUL 2004
COPYRIGHT (C) 2004 THOMSON DERWENT

FILE 'PROMT' ENTERED AT 19:35:08 ON 28 JUL 2004
COPYRIGHT (C) 2004 Gale Group. All rights reserved.

FILE 'EMBASE' ENTERED AT 19:35:08 ON 28 JUL 2004
COPYRIGHT (C) 2004 Elsevier Inc. All rights reserved.

FILE 'CEABA-VTB' ENTERED AT 19:35:08 ON 28 JUL 2004
COPYRIGHT (c) 2004 DECHEMA eV

FILE 'MEDLINE' ENTERED AT 19:35:08 ON 28 JUL 2004

FILE 'SCISEARCH' ENTERED AT 19:35:08 ON 28 JUL 2004
COPYRIGHT 2004 THOMSON ISI

FILE 'CAPLUS' ENTERED AT 19:35:08 ON 28 JUL 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'PASCAL' ENTERED AT 19:35:08 ON 28 JUL 2004
Any reproduction or dissemination in part or in full,
by means of any process and on any support whatsoever
is prohibited without the prior written agreement of INIST-CNRS.
COPYRIGHT (C) 2004 INIST-CNRS. All rights reserved.

FILE 'BIOSIS' ENTERED AT 19:35:08 ON 28 JUL 2004
COPYRIGHT (C) 2004 BIOLOGICAL ABSTRACTS INC.(R)

FILE 'USPATFULL' ENTERED AT 19:35:08 ON 28 JUL 2004
CA INDEXING COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'ESBIOBASE' ENTERED AT 19:35:08 ON 28 JUL 2004
COPYRIGHT (C) 2004 Elsevier Science B.V., Amsterdam. All rights reserved.

=> s (helicas? or mtt1?) and (erf? or (releas?(s)facto?))
   8 FILES SEARCHED...
L2          673 (HELICAS? OR MTT1?) AND (ERF? OR (RELEAS?(S) FACTO?))

=> s l2 and (upf? or nam7? or sal1? or ifs2? or mof4? or nmd2? or isf1? or sua1? or sua6?)
L3           51 L2 AND (UPF? OR NAM7? OR SAL1? OR IFS2? OR MOF4? OR NMD2? OR
                ISF1? OR SUA1? OR SUA6?)

=> dup rem l3
DUPLICATE IS NOT AVAILABLE IN 'DGENE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L3
L4           46 DUP REM L3 (5 DUPLICATES REMOVED)

=> d ti l4 1-46

L4   ANSWER 1 OF 46  USPATFULL on STN
TI     Methods for in vitro expansion and transdifferentiation of human
       pancreatic acinar cells into insulin-producing cells

L4   ANSWER 2 OF 46  USPATFULL on STN
TI     Ncc2705-the genome of a bifodobacterium

L4   ANSWER 3 OF 46  USPATFULL on STN
```

TI Subfamily of RNA **helicases** which are modulators of the fidelity of translation termination and uses thereof

L4 ANSWER 4 OF 46 USPATFULL on STN
TI Targets for therapeutic intervention identified in the mitochondrial proteome

L4 ANSWER 5 OF 46 USPATFULL on STN
TI Whole cell engineering by mutagenizing a substantial portion of a starting genome, combining mutations, and optionally repeating

L4 ANSWER 6 OF 46 USPATFULL on STN
TI Methods of identifying compounds that inhibit nonstop degradation of mRNA

L4 ANSWER 7 OF 46 USPATFULL on STN
TI Wound healing biomarkers

L4 ANSWER 8 OF 46 USPATFULL on STN
TI Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer

L4 ANSWER 9 OF 46 USPATFULL on STN
TI Composition for the detection of signaling pathway gene expression

L4 ANSWER 10 OF 46 USPATFULL on STN
TI Novel human polynucleotides and polypeptides encoded thereby

L4 ANSWER 11 OF 46 USPATFULL on STN
TI Methods of diagnosis of ovarian cancer, compositions and methods of screening for modulators of ovarian cancer

L4 ANSWER 12 OF 46 USPATFULL on STN
TI Novel full-length cDNA

L4 ANSWER 13 OF 46 USPATFULL on STN
TI Nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics

L4 ANSWER 14 OF 46 USPATFULL on STN
TI Nucleic acid molecule and encoded protein associated with sterol synthesis and metabolism

L4 ANSWER 15 OF 46 USPATFULL on STN
TI DNA array sequence selection

L4 ANSWER 16 OF 46 MEDLINE on STN
TI Leaky termination at premature stop codons antagonizes nonsense-mediated mRNA decay in S. cerevisiae.

L4 ANSWER 17 OF 46 USPATFULL on STN
TI Novel full length cDNA

L4 ANSWER 18 OF 46 USPATFULL on STN
TI Novel methods of diagnosis of metastatic colorectal cancer, compositions and methods of screening for modulators of metastatic colorectal cancer

L4 ANSWER 19 OF 46 USPATFULL on STN
TI Protein-protein interactions in adipocyte cells (3)

L4 ANSWER 20 OF 46 USPATFULL on STN
TI Novel full-length cDNA

L4 ANSWER 21 OF 46 USPATFULL on STN
TI Segments of the human gene for telomerase reverse transcriptase

L4 ANSWER 22 OF 46 USPATFULL on STN
TI Yeast proteome analysis

L4 ANSWER 23 OF 46 USPATFULL on STN
TI Novel nucleic acids and polypeptides

L4 ANSWER 24 OF 46 USPATFULL on STN
TI Libraries of expressible gene sequences

L4 ANSWER 25 OF 46 USPATFULL on STN
TI Methods of diagnosis of ovarian cancer, compositions and methods of screening for modulators of ovarian cancer

L4 ANSWER 26 OF 46 USPATFULL on STN
TI Libraries of expressible gene sequences

L4 ANSWER 27 OF 46 USPATFULL on STN
TI Human genes and gene expression products

L4 ANSWER 28 OF 46 USPATFULL on STN
TI Protein-protein interactions in adipocyte cells

L4 ANSWER 29 OF 46 USPATFULL on STN
TI Method of modulating the efficiency of translation termination and degradation of aberrant mRNA involving a surveillance complex comprising human **Upf1p**,eucaryotic **release factor** 1 and eucaryotic **release factor** 3

L4 ANSWER 30 OF 46 USPATFULL on STN
TI Subfamily of RNA **helicases** which are modulators of the fidelity of translation termination and uses thereof

L4 ANSWER 31 OF 46 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Enterococcus faecalis for diagnostics and therapeutics

L4 ANSWER 32 OF 46 USPATFULL on STN
TI Cells immortalized with telomerase reverse transcriptase for use in drug screening

L4 ANSWER 33 OF 46 USPATFULL on STN
TI Promoter for telomerase reverse transcriptase

L4 ANSWER 34 OF 46 USPATFULL on STN
TI ENTEROCOCCUS FAECALIS POLYNUCLEOTIDES AND POLYPEPTIDES

L4 ANSWER 35 OF 46 USPATFULL on STN
TI Composition for the detection of signaling pathway gene expression

L4 ANSWER 36 OF 46 USPATFULL on STN
TI METHOD OF MODULATING THE EFFICIENCY OF TRANSLATION TERMINATION AND DEGRADATION OF ABERRANT MRNA INVOLVING A SURVEILLANCE COMPLEX COMPRISING HUMAN **UPF1P**, EUCARYOTIC **RELEASE FACTOR** 1 AND EUCARYOTIC **RELEASE FACTOR** 3

L4 ANSWER 37 OF 46 USPATFULL on STN
TI Polynucleotides and polypeptides derived from corn ear

L4 ANSWER 38 OF 46 USPATFULL on STN
TI Genomic DNA sequences of ashbya gossypii and uses thereof

L4 ANSWER 39 OF 46 CAPLUS COPYRIGHT 2004 ACS on STN
TI Subfamily of RNA **helicases** which are modulators of the fidelity of translation termination

L4 ANSWER 40 OF 46 USPATFULL on STN
TI Telomerase catalytic subunit

L4 ANSWER 41 OF 46 MEDLINE on STN DUPLICATE 1
TI **Mtt1** is a **Upf1**-like **helicase** that interacts with the translation termination factors and whose overexpression can modulate termination efficiency.

L4 ANSWER 42 OF 46 MEDLINE on STN
TI RNA surveillance. Unforeseen consequences for gene expression, inherited genetic disorders and cancer.

L4 ANSWER 43 OF 46 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN DUPLICATE 2
TI A mutated human homologue to yeast **Upf1** protein has a dominant-negative effect on the decay of nonsense-containing mRNAs in mammalian cells.

L4 ANSWER 44 OF 46 MEDLINE on STN
TI The surveillance complex interacts with the translation **release factors** to enhance termination and degrade aberrant mRNAs.

L4 ANSWER 45 OF 46 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
TI PURIFICATION AND CHARACTERIZATION OF THE **UPF1** PROTEIN - A FACTOR INVOLVED IN TRANSLATION AND MESSENGER-RNA DEGRADATION

L4 ANSWER 46 OF 46 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy -

=> d ibib abs l4 29 30 36 39 43 44 46

L4 ANSWER 29 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2003:44848 USPATFULL
TITLE: Method of modulating the efficiency of translation termination and degradation of aberrant mRNA involving a surveillance complex comprising human **Upf1p** ,eucaryotic **release factor** 1 and eucaryotic **release factor** 3
INVENTOR(S): Peltz, Stuart, Piscataway, NJ, UNITED STATES
Czaplinski, Kevin, Somerset, NJ, UNITED STATES
Weng, Youmin, Cranford, NJ, UNITED STATES
PATENT ASSIGNEE(S): University of Medicine and Dentistry of New Jersey, New Brunswick, NY, UNITED STATES, 08903 (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003032158	A1	20030213
APPLICATION INFO.:	US 2002-138784	A1	20020503 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1999-321649, filed on 28 May 1999, ABANDONED

	NUMBER	DATE
PRIORITY INFORMATION:	US 1998-86986P	19980528 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: PERKINS COIE LLP, POST OFFICE BOX 1208, SEATTLE, WA, 98111-1208
NUMBER OF CLAIMS: 28
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Page(s)
LINE COUNT: 2935
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Provided are novel methods and assays to identify agents and compositions that modulate the ability of the eukaryotic surveillance complex to effect translation termination and degradation of aberrant mRNA.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 30 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2003:268126 USPATFULL
TITLE: Subfamily of RNA **helicases** which are modulators of the fidelity of translation termination and uses thereof
INVENTOR(S): Peltz, Stuart, Piscataway, NJ, United States
Czaplinski, Kevin, Somerset, NJ, United States
Dinman, Jonathan D., North Brunswick, NJ, United States
PATENT ASSIGNEE(S): University of Medicine and Dentistry of New Jersey, New

Brunswick, NJ, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6630294	B1	20031007
APPLICATION INFO.:	US 1999-359268		19990722 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1998-93685P	19980722 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Prouty, Rebecca E.
ASSISTANT EXAMINER: Ramirez, Delia
LEGAL REPRESENTATIVE: Wise, Michael J., Perkins Coie LLP
NUMBER OF CLAIMS: 4
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 6 Drawing Figure(s); 6 Drawing Page(s)
LINE COUNT: 2768
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention provides a method for modulating the efficiency of translation termination of messenger RNA. Also provided are methods of screening for compositions and agents capable of modulating translation termination.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 36 OF 46 USPATFULL on STN
ACCESSION NUMBER: 2002:311029 USPATFULL
TITLE: METHOD OF MODULATING THE EFFICIENCY OF TRANSLATION TERMINATION AND DEGRADATION OF ABERRANT MRNA INVOLVING A SURVEILLANCE COMPLEX COMPRISING HUMAN **UPF1P**, EUCARYOTIC **RELEASE FACTOR** 1 AND EUCARYOTIC **RELEASE FACTOR** 3
INVENTOR(S): Peltz, Stuart, 67 Castle Pointe Blvd., Piscataway, NJ, United States 08854
Czaplinski, Kevin, 115 Hollywood Ave., Somerset, NJ, United States 08873
Weng, Youmin, 2 Indian Spring Rd., Cranford, NJ, United States 07016

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6486305	B1	20021126
APPLICATION INFO.:	US 2000-639987		20000816 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1998-86260, filed on 28 May 1998, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: McCarry, Sean
ASSISTANT EXAMINER: Zara, Jane
LEGAL REPRESENTATIVE: Lyon & Lyon LLP
NUMBER OF CLAIMS: 3
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 2808
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention provides a method of modulating translation termination efficiency of mRNA and/or promoting degradation of abberant transcripts. Also, this invention provides a method of screening for a drug active involved in enhancing translation termination and a method for identifying a disease state involving defective the protein complex.

This invention provides a purified complex comprising an amount of a human **Upf1p** protein, a peptidyl eucaryotic **release factor** 1 (**eRF1**) and a peptidyl eucaryotic **release factor** 3 (**eRF3**) effective to modulate translation termination. Further, this invention provides an expression vector which comprises a nucleic acid encoding a human **Upf1p** protein, a peptidyl eucaryotic **release factor** 1 (**eRF1**) and a peptidyl eucaryotic

release factor 3 (**eRF3**) operably linked to a regulatory element.

This invention provides an antibody which binds to the complex comprising an amount of a human **Upf1p** protein, a peptidyl eucaryotic **release factor** 1 (**eRF1**) and a peptidyl eucaryotic **release factor** 3 (**eRF3**) effective to modulate translation termination. This invention provides an agent which inhibits or modulates the binding of human **Upf1p** to **eRF1** or **eRF3** The agent may inhibit or facilitate the binding of human **Upf1p** to **eRF1** or **eRF3** .

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 39 OF 46 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:85103 CAPLUS
DOCUMENT NUMBER: 132:148498
TITLE: Subfamily of RNA **helicases** which are modulators of the fidelity of translation termination
INVENTOR(S): Peltz, Stuart; Czaplinski, Kevin; Dinman, Jonathan D.
PATENT ASSIGNEE(S): University of Medicine and Dentistry, USA
SOURCE: PCT Int. Appl., 89 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000005586	A2	20000203	WO 1999-US16802	19990722
WO 2000005586	A3	20000420		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2338312	AA	20000203	CA 1999-2338312	19990722
AU 9952286	A1	20000214	AU 1999-52286	19990722
EP 1098905	A2	20010516	EP 1999-937450	19990722
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002524719	T2	20020806	JP 2000-561501	19990722

PRIORITY APPLN. INFO.: US 1998-120435 A2 19980722
WO 1999-US16802 W 19990722

AB This invention provides a method of modulating translation termination efficiency of mRNA and/or promoting degrdn. of aberrant transcripts. Also, this invention provides a method of screening for a drug active involved in enhancing translation termination and a method for identifying a disease state involving defective the protein complex. This invention provides a purified complex comprising an amt. of **MTT1** (mediator of translation termination, the gene encoding **helicase** B), human **Upf1p**, a peptidyl eukaryotic **release factor** 1 (**eRF1**) and a peptidyl eukaryotic **release factor** 3 (**eRF3**) effective to modulate translation termination. Further, this invention provides an expression vector which comprises a nucleic acid encoding a **MTT1**, a human **Upf1p** protein, a peptidyl eukaryotic **release factor** 1 (**eRF1**) and a peptidyl eukaryotic **release factor** 3 (**eRF3**) operably linked to a regulatory element. This invention provides an antibody which binds to the complex comprising an amt. of a **MTT1**, human **Upf1p** protein, a peptidyl eukaryotic **release factor** 1 (**eRF1**) and a peptidyl eukaryotic **release factor** 3 (**eRF3**) effective to modulate translation termination. This invention provides an agent which inhibits or modulates the binding of **MTT1** to

eRF3. The agent may inhibit or facilitate the binding of **MTT1** to **eRF3**. Alignment of several RNA **helicases** identifies 9 motifs characteristic of modulators of translation termination.

L4 ANSWER 43 OF 46 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 2

ACCESSION NUMBER: 1998305591 EMBASE
TITLE: A mutated human homologue to yeast **Upf1** protein has a dominant-negative effect on the decay of nonsense-containing mRNAs in mammalian cells.
AUTHOR: Sun X.; Perlick H.A.; Dietz H.C.; Maquat L.E.
CORPORATE SOURCE: L.E. Maquat, Roswell Park Cancer Institute, Department of Genetics, Elm and Carlton Streets, Buffalo, NY 14263, United States. maquat@sc3101.med.buffalo.edu
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (18 Aug 1998) 95/17 (10009-10014).
Refs: 46
ISSN: 0027-8424 CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB All eukaryotic cells analyzed have developed mechanisms to eliminate the production of mRNAs that prematurely terminate translation. The mechanisms are thought to exist to protect cells from the deleterious effects of in-frame nonsense codons that are generated by routine inefficiencies and inaccuracies in RNA metabolism such as pre-mRNA splicing. Depending on the particular mRNA and how it is produced, nonsense codons can mediate a reduction in mRNA abundance either (i) before its **release** from an association with nuclei into the cytoplasm, presumably but not certainly while the mRNA is being exported to the cytoplasm and translated by cytoplasmic ribosomes, or (ii) in the cytoplasm. Here, we provide evidence for a **factor** that functions to eliminate the production of nonsense-containing RNAs in mammalian cells. The **factor**, variously referred to as Rent1 (regulator of nonsense transcripts) or HUPF1 (human **Upf1** protein), was identified by isolating cDNA for a human homologue to Saccharomyces cerevisiae **Upf1p**, which is a group I RNA **helicase** that functions in the nonsenser mediated decay of mRNA in yeast. Using monkey COS cells and human HeLa cells, we demonstrate that expression of human **Upf1** protein harboring an arginine-to-cysteine mutation at residue 844 within the RNA **helicase** domain acts in a dominant- negative fashion to abrogate the decay of nonsense-containing mRNA that takes place (i) in association with nuclei or (ii) in the cytoplasm. These findings provide evidence that nonsense-mediated mRNA decay is related mechanistically in yeast and in mammalian cells, regardless of the cellular site of decay.

L4 ANSWER 44 OF 46 MEDLINE on STN

ACCESSION NUMBER: 1998283914 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9620853
TITLE: The surveillance complex interacts with the translation **release factors** to enhance termination and degrade aberrant mRNAs.
AUTHOR: Czaplinski K; Ruiz-Echevarria M J; Paushkin S V; Han X; Weng Y; Perlick H A; Dietz H C; Ter-Avanesyan M D; Peltz S W
CORPORATE SOURCE: Department of Molecular Genetics and Microbiology, Robert Wood Johnson Medical School-UMDNJ, USA.
CONTRACT NUMBER: GM48631-01 (NIGMS)
SOURCE: Genes & development, (1998 Jun 1) 12 (11) 1665-77.
Journal code: 8711660. ISSN: 0890-9369.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980713
Last Updated on STN: 19980713

Entered Medline: 19980701

AB The nonsense-mediated mRNA decay pathway is an example of an evolutionarily conserved surveillance pathway that rids the cell of transcripts that contain nonsense mutations. The product of the **UPF1** gene is a necessary component of the putative surveillance complex that recognizes and degrades aberrant mRNAs. Recent results indicate that the **Upf1p** also enhances translation termination at a nonsense codon. The results presented here demonstrate that the yeast and human forms of the **Upf1p** interact with both eukaryotic translation termination factors **eRF1** and **eRF3**. Consistent with **Upf1p** interacting with the **eRFs**, the **Upf1p** is found in the prion-like aggregates that contain **eRF1** and **eRF3** observed in yeast [PSI+] strains. These results suggest that interaction of the **Upf1p** with the peptidyl **release factors** may be a key event in the assembly of the putative surveillance complex that enhances translation termination, monitors whether termination has occurred prematurely, and promotes degradation of aberrant transcripts.

L4 ANSWER 46 OF 46 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: AAY77814 peptide DGENE
TITLE: New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy -
INVENTOR: Peltz S; Czaplinski K; Dinman J D
PATENT ASSIGNEE: (UYNE-N)UNIV NEW JERSEY.
PATENT INFO: WO 2000005586 A2 20000203 89p
APPLICATION INFO: WO 1999-US16802 19990722
PRIORITY INFO: US 1998-120435 19980722
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2000-171458 [15]
DESCRIPTION: Yeast **Upf1** protein fragment.
AN AAY77814 peptide DGENE
AB The invention provides a new multiprotein complex which can modulate peptidyl transferase activity during translation. The complex comprises the gene encoding **Helicase** B (HCSB; renamed **MTT1**, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl eukaryotic **release factor** (**eRF**) 1 and **eRF3**. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker Muscular Dystrophy etc. It can be used to identify disease conditions involving a defect in the complex, by transfecting cells with encoding nucleic acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved in peptidyl transferase activity during translation, inhibiting the interaction between **MTT1** and **eRF3** or involved in enhancing translation termination. Vectors comprising polynucleotides encoding the complex (or antisense sequences) can be constructed and introduced into cells to interfere with complex expression and so modulate the efficiency of translation termination of mRNA and/or degradation of aberrant transcripts in a cell. Agents binding to the complex can be identified and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They are also useful to modulate the efficiency of translation termination of mRNA at a nonsense codon and/or promote degradation of aberrant transcripts in cells. The method can be used to identify agents/ compositions modulating binding to **MTT1** , useful to identify genes. Sequences AAY77813-817 represent protein fragments from yeast superfamily group I **helicases**.

=> dhis
DHIS IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter

"HELP COMMANDS" at an arrow prompt (=>).

=> d his

(FILE 'HOME' ENTERED AT 19:31:12 ON 28 JUL 2004)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 19:31:26 ON 28 JUL 2004

SEA (HELICAS? OR MTT1?) OR (ERF? OR (RELEAS?(S)FACTO?))

1596	FILE ADISCTI
354	FILE ADISINSIGHT
378	FILE ADISNEWS
6851	FILE AGRICOLA
192	FILE ANABSTR
2954	FILE AQUASCI
1469	FILE BIOBUSINESS
234	FILE BIOCOMMERCE
43311	FILE BIOSIS
2564	FILE BIOTECHABS
2564	FILE BIOTECHDS
25707	FILE BIOTECHNO
14587	FILE CABA
22758	FILE CANCERLIT
50487	FILE CAPLUS
60171	FILE CEABA-VTB
83	FILE CEN
444	FILE CIN
1196	FILE CONFSCI
306	FILE CROPB
455	FILE CROPU
4438	FILE DISSABS
10295	FILE DDFB
18653	FILE DDFU
399612	FILE DGENE
10295	FILE DRUGB
41	FILE DRUGMONOG2
183	FILE IMSDRUGNEWS
21744	FILE DRUGU
192	FILE IMSRESEARCH
721	FILE EMBAL
83157	FILE EMBASE
27817	FILE ESBIOBASE
3955*	FILE FEDRIP
304	FILE FOMAD
475	FILE FROSTI
1816	FILE FSTA
17804	FILE GENBANK
453	FILE HEALSAFE
3074	FILE IFIPAT
72	FILE IMSPRODUCT
4377	FILE JICST-EPLUS
246	FILE KOSMET
20977	FILE LIFESCI
76	FILE MEDICONF
59476	FILE MEDLINE
844	FILE NIOSHTIC
3489	FILE NTIS
11	FILE NUTRACEUT
754	FILE OCEAN
44363	FILE PASCAL
431	FILE PHAR
130	FILE PHARMAML
5	FILE PHIC
788	FILE PHIN
304170	FILE PROMT
1131	FILE PROUSDDR
475	FILE RDISCLOSURE

```
            58511   FILE SCISEARCH
               10   FILE SYNTHLINE
            20905   FILE TOXCENTER
            43056   FILE USPATFULL
             2544   FILE USPAT2
              829   FILE VETB
             2402   FILE VETU
             4638   FILE WPIDS
             1925   FILE WPIFV
             4638   FILE WPINDEX
              944   FILE IPA
              171   FILE NAPRALERT
            19988   FILE NLDB
L1               QUE (HELICAS? OR MTT1?) OR (ERF? OR (RELEAS?(S) FACTO?))
                 ---------

     FILE 'DGENE, PROMT, EMBASE, CEABA-VTB, MEDLINE, SCISEARCH, CAPLUS,
     PASCAL, BIOSIS, USPATFULL, ESBIOBASE' ENTERED AT 19:35:08 ON 28 JUL 2004
L2            673 S (HELICAS? OR MTT1?) AND (ERF? OR (RELEAS?(S)FACTO?))
L3             51 S L2 AND (UPF? OR NAM7? OR SAL1? OR IFS2? OR MOF4? OR NMD2? OR
L4             46 DUP REM L3 (5 DUPLICATES REMOVED)

=> log h
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                    60.31      63.94

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                       ENTRY    SESSION
CA SUBSCRIBER PRICE                                    -0.74      -0.74

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 19:44:34 ON 28 JUL 2004
```

1: NP_542199. UPF3 regulator of...[gi:18375528] BLink, Domains, Links

```
LOCUS       NP_542199                 483 aa            linear   PRI 21-DEC-2003
DEFINITION  UPF3 regulator of nonsense transcripts homolog B isoform 1 [Homo
            sapiens].
ACCESSION   NP_542199
VERSION     NP_542199.1  GI:18375528
DBSOURCE    REFSEQ: accession NM_080632.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 483)
  AUTHORS   Gehring,N.H., Neu-Yilik,G., Schell,T., Hentze,M.W. and Kulozik,A.E.
  TITLE     Y14 and hUpf3b form an NMD-activating complex
  JOURNAL   Mol. Cell 11 (4), 939-949 (2003)
   PUBMED   12718880
  REMARK    GeneRIF: A conserved domain of hUpf3b mediates an interaction with
            the EJC protein Y14. Y14 is required for nonsense-mediated decay
            induced by tethered hUpf3b.
REFERENCE   2  (residues 1 to 483)
  AUTHORS   Lykke-Andersen,J., Shu,M.D. and Steitz,J.A.
  TITLE     Communication of the position of exon-exon junctions to the mRNA
            surveillance machinery by the protein RNPS1
  JOURNAL   Science 293 (5536), 1836-1839 (2001)
   PUBMED   11546874
  REMARK    GeneRIF: binds RNPS1 protein, part of the postsplicing complex
            deposited 5' to exon-exon junctions
REFERENCE   3  (residues 1 to 483)
  AUTHORS   Kim,V.N., Kataoka,N. and Dreyfuss,G.
  TITLE     Role of the nonsense-mediated decay factor hUpf3 in the
            splicing-dependent exon-exon junction complex
  JOURNAL   Science 293 (5536), 1832-1836 (2001)
   PUBMED   11546873
  REMARK    GeneRIF: binds to spliced mRNAs upstream of exon-exon junctions; is
            part of mRNP complexes that are ready for nuclear export and that
            participate in nonsense-mediated mRNA decay
REFERENCE   4  (residues 1 to 483)
  AUTHORS   Serin,G., Gersappe,A., Black,J.D., Aronoff,R. and Maquat,L.E.
  TITLE     Identification and characterization of human orthologues to
            Saccharomyces cerevisiae Upf2 protein and Upf3 protein
            (Caenorhabditis elegans SMG-4)
  JOURNAL   Mol. Cell. Biol. 21 (1), 209-223 (2001)
   PUBMED   11113196
REFERENCE   5  (residues 1 to 483)
  AUTHORS   Lykke-Andersen,J., Shu,M.D. and Steitz,J.A.
  TITLE     Human Upf proteins target an mRNA for nonsense-mediated decay when
            bound downstream of a termination codon
  JOURNAL   Cell 103 (7), 1121-1131 (2000)
   PUBMED   11163187
```

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AF318576.1, AY013251.1 and BI549935.1.

Summary: This gene encodes a protein that is part of a post-splicing multiprotein complex involved in both mRNA nuclear export and mRNA surveillance. The encoded protein is one of two functional homologs to yeast Upf3p. mRNA surveillance detects exported mRNAs with truncated open reading frames and initiates nonsense-mediated mRNA decay (NMD). When translation ends upstream from the last exon-exon junction, this triggers NMD to degrade mRNAs containing premature stop codons. This protein binds to the mRNA and remains bound after nuclear export, acting as a nucleocytoplasmic shuttling protein. It forms with Y14 a complex that binds specifically 20 nt upstream of exon-exon junctions. This gene is located on the long arm of chromosome X. Two splice variants encoding different isoforms have been found for this gene.

Transcript Variant: This variant (1) contains exon 8 and encodes the longer isoform (1), also known as hUpf3-X.

FEATURES Location/Qualifiers

source 1..483
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xq25-q26"

Protein 1..483
/product="UPF3 regulator of nonsense transcripts homolog B isoform 1"

Region 44..206
/region_name="Smg-4/UPF3 family"
/note="Smg4_UPF3"
/db_xref="CDD:23456"

Region <428..481
/region_name="Nonsense-mediated decay protein Upf3 [RNA processing and modification]"
/note="KOG1295"
/db_xref="CDD:19084"

CDS 1..483
/gene="UPF3B"
/coded_by="NM_080632.1:78..1529"
/note="isoform 1 is encoded by transcript variant 1"
/db_xref="GeneID:65109"
/db_xref="LocusID:65109"
/db_xref="MIM:300298"

ORIGIN

```
        1 mkeekehrpk ekrvtlltpa gatgsgggts gdsskgedkq drnkekkeal skvvirrlpp
       61 tltkeqlqeh lqpmpehdyf effsndtsly phmyarayin fknqediilf rdrfdgyvfl
      121 dnkgqeypai vefapfqkaa kkktkkrdtk vgtidddpey rkflesyatd nekmtstpet
      181 lleeieaknr eliakkttpl lsflknkqrm reekreerrr reierkrqre eerrkwkeee
      241 krkrkdiekl kkidriperd klkdepkikv hrfllqavnq knllkkpekg dekeldkrek
      301 akkldkenls derasgqsct lpkrsdselk dekpkrpede sgrdyrerer eyerdqeril
      361 rererlkrqe eerrrqkery ekektfkrke eemkkekdtl rdkgkkaest esigssekte
      421 kkeevvkrdr irnkdrpamq lyqpgarsrn rlcppddstk sgdsaaerkq esgishrkeg
      481 gee
//
```

1: NP_542166. UPF2 regulator of...[gi:18375676] BLink, Domains, Links

LOCUS NP_542166 1272 aa linear PRI 21-DEC-2003
DEFINITION UPF2 regulator of nonsense transcripts homolog; regulator of nonsense transcripts 2; yeast Upf2p homolog [Homo sapiens].
ACCESSION NP_542166
VERSION NP_542166.1 GI:18375676
DBSOURCE REFSEQ: accession NM_080599.1
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 1272)
AUTHORS Serin,G., Gersappe,A., Black,J.D., Aronoff,R. and Maquat,L.E.
TITLE Identification and characterization of human orthologues to Saccharomyces cerevisiae Upf2 protein and Upf3 protein (Caenorhabditis elegans SMG-4)
JOURNAL Mol. Cell. Biol. 21 (1), 209-223 (2001)
PUBMED 11113196
REFERENCE 2 (residues 1 to 1272)
AUTHORS Lykke-Andersen,J., Shu,M.D. and Steitz,J.A.
TITLE Human Upf proteins target an mRNA for nonsense-mediated decay when bound downstream of a termination codon
JOURNAL Cell 103 (7), 1121-1131 (2000)
PUBMED 11163187
REFERENCE 3 (residues 1 to 1272)
AUTHORS Mendell,J.T., Medghalchi,S.M., Lake,R.G., Noensie,E.N. and Dietz,H.C.
TITLE Novel Upf2p orthologues suggest a functional link between translation initiation and nonsense surveillance complexes
JOURNAL Mol. Cell. Biol. 20 (23), 8944-8957 (2000)
PUBMED 11073994
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AB037829.1 and AW444636.1.

Summary: This gene encodes a protein that is part of a post-splicing multiprotein complex involved in both mRNA nuclear export and mRNA surveillance. mRNA surveillance detects exported mRNAs with truncated open reading frames and initiates nonsense-mediated mRNA decay (NMD). When translation ends upstream from the last exon-exon junction, this triggers NMD to degrade mRNAs containing premature stop codons. This protein is located in the perinuclear area. It interacts with translation release factors and the proteins that are functional homologs of yeast Upf1p and Upf3p. Two splice variants have been found for this gene; both variants encode the same protein.

Transcript Variant: This variant (1) contains a different 5' UTR than variant 2 and is the longer transcript.
FEATURES Location/Qualifiers

```
     source          1..1272
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10p14-p13"
     Protein         1..1272
                     /product="UPF2 regulator of nonsense transcripts homolog"
                     /note="regulator of nonsense transcripts 2; yeast Upf2p
                     homolog"
     Region          140..>1024
                     /region_name="Nonsense-mediated mRNA decay 2 protein [RNA
                     processing and modification]"
                     /note="KOG2051"
                     /db_xref="CDD:19837"
     Region          168..>320
                     /region_name="MIF4G domain"
                     /note="MIF4G"
                     /db_xref="CDD:23388"
     Region          571..758
                     /region_name="MIF4G domain"
                     /note="MIF4G"
                     /db_xref="CDD:23388"
     Region          773..986
                     /region_name="MIF4G domain"
                     /note="MIF4G"
                     /db_xref="CDD:23388"
     Region          <1076..1220
                     /region_name="Up-frameshift suppressor 2"
                     /note="Upf2"
                     /db_xref="CDD:9609"
     Region          <1095..1266
                     /region_name="Nonsense-mediated mRNA decay 2 protein [RNA
                     processing and modification]"
                     /note="KOG2051"
                     /db_xref="CDD:19837"
     CDS             1..1272
                     /gene="UPF2"
                     /coded_by="NM_080599.1:130..3948"
                     /note="go_function: RNA binding [goid 0003723] [evidence
                     IEA];
                     go_process: protein biosynthesis [goid 0006412] [evidence
                     IEA]"
                     /db_xref="GeneID:26019"
                     /db_xref="LocusID:26019"
                     /db_xref="MIM:605529"
ORIGIN
        1 mpaerkkpas meekdslpnn kekdcserrt vsskerpkdd ikltakkevs kapedkkkrl
       61 eddkrkkedk erkkkdeekv kaeeeskkke eeekkkhqee erkkqeeqak rqqeeeaaaq
      121 mkekeesiql hqeawerhhl rkelrsknqn apdsrpeenf fsrldsslkk ntafvkklkt
      181 iteqqrdsls hdfnglnlsk yiaeavasiv eaklkisdvn cavhlcslfh qryadfapsl
      241 lqvwkkhfea rkeektpnit klrtdlrfia eltivgiftd keglsliyeq lkniinadre
      301 shthvsvvis fcrhcgddia glvprkvksa aekfnlsfpp seiispekqq pfqnllkeyf
      361 tsltkhlkrd hrelqnterq nrrilhskge lsedrhkqye efamsyqkll ansqsladll
      421 denmpdlpqd kptpeehgpg idiftpgkpg eydleggiwe dedarnfyen lidlkafvpa
      481 ilfkdneksc qnkesnkddt keakeskenk evsspddlel elenleindd tleleggdea
      541 edltkkllde qeqedeeast gshlklivda flqqlpncvn rdlidkaamd fcmnmntkan
      601 rkklvralfi vprqrldllp fyarlvatlh pcmsdvaedl csmlrgdfrf hvrkkdqini
      661 etknktvrfi geltkfkmft kndtlhclkm llsdfshhhi emactlletc grflfrspes
      721 hlrtsvlleq mmrkkqamhl daryvtmven ayyycnpppa ektvkkkrpp lqeyvrklly
      781 kdlskvttek vlrqmrklpw qdqevkdyvi ccminiwnvk ynsihcvanl laglvlyqed
```

```
      841 vgihvvdgvl edirlgmevn qpkfnqrris sakflgelyn yrmvesavif rtlysftsfg
      901 vnpdgspssl dppehlfrir lvctildtcg qyfdrgsskr kldcflvyfq ryvwwkksle
      961 vwtkdhpfpi didymisdtl ellrpkiklc nsleesirqv qdlereflik lglvndkdsk
     1021 dsmtegenle edeeeeegga eteeqsgnes evnepeeeeg sdndddegee eeeentdylt
     1081 dsnkenetde entevmikgg glkhvpcved edfiqaldkm mlenlqqrsg esvkvhqldv
     1141 aiplhlksql rkgpplggge geaesadtmp fvmltrkgnk qqfkilnvpm ssqlaanhwn
     1201 qqqaeqeerm rmkkltldin erqeqedyqe mlqslaqrpa pantnrerrp ryqhpkgapn
     1261 adlifktggr rr
//
```

1: NP_060564. peptide chain rel...[gi:46094014] BLink, Domains, Links

```
LOCUS       NP_060564                628 aa            linear   PRI 12-JUL-2004
DEFINITION  peptide chain release factor 3 [Homo sapiens].
ACCESSION   NP_060564
VERSION     NP_060564.2  GI:46094014
DBSOURCE    REFSEQ: accession NM_018094.2
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 628)
  AUTHORS   Hansen,L.L., Jakobsen,C.G. and Justesen,J.
  TITLE     Assignment of the human peptide chain release factor 3 (GSPT2) to
            Xp11.23-->p11.21 and of the distal marker DXS1039 by radiation
            hybrid mapping
  JOURNAL   Cytogenet. Cell Genet. 86 (3-4), 250-251 (1999)
   PUBMED   10575220
REFERENCE   2  (residues 1 to 628)
  AUTHORS   Hoshino,S., Imai,M., Mizutani,M., Kikuchi,Y., Hanaoka,F., Ui,M. and
            Katada,T.
  TITLE     Molecular cloning of a novel member of the eukaryotic polypeptide
            chain-releasing factors (eRF). Its identification as eRF3
            interacting with eRF1
  JOURNAL   J. Biol. Chem. 273 (35), 22254-22259 (1998)
   PUBMED   9712840
COMMENT     VALIDATED REFSEQ: This record has undergone preliminary review of
            the sequence, but has not yet been subject to final review. The
            reference sequence was derived from BC036077.1, AJ251548.1,
            AK001303.1 and AK023155.1.
            On Apr 2, 2004 this sequence version replaced gi:8922424.

            Summary: GSPT2 is closely related to GSPT1 (MIM 139259), a
            GTP-binding protein that plays an essential role at the G1- to
            S-phase transition of the cell cycle in yeast and human cells.
            GSPT1 is a positive regulator of translational accuracy and, in a
            binary complex with eRF1 (MIM 600285), functions as a polypeptide
            chain release factor. [supplied by OMIM].
FEATURES             Location/Qualifiers
     source          1..628
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xp11.23-p11.21"
     Protein         1..628
                     /product="peptide chain release factor 3"
     Region          201..625
                     /region_name="Translation elongation factor EF-1alpha
                     (GTPase) [Translation, ribosomal structure and
                     biogenesis]"
```

```
                     /note="TEF1"
                     /db_xref="CDD:14378"
     Region          201..418
                     /region_name="Elongation factor Tu GTP binding domain"
                     /note="GTP_EFTU"
                     /db_xref="CDD:22868"
     Region          443..510
                     /region_name="Elongation factor Tu domain 2"
                     /note="GTP_EFTU_D2"
                     /db_xref="CDD:24678"
     Region          522..624
                     /region_name="Elongation factor Tu C-terminal domain"
                     /note="GTP_EFTU_D3"
                     /db_xref="CDD:23422"
     CDS             1..628
                     /gene="GSPT2"
                     /coded_by="NM_018094.2:197..2083"
                     /note="go_function: GTP binding [goid 0005525] [evidence
                     IEA];
                     go_process: protein biosynthesis [goid 0006412] [evidence
                     IEA]"
                     /db_xref="GeneID:23708"
                     /db_xref="LocusID:23708"
                     /db_xref="MIM:300418"
ORIGIN
        1 mdsgssssds apdcwdqvdm espgsapsgd gvssavaeaq replssafsr klnvnakpfv
       61 pnvhaaefvp sflrgptqpp tlpagsgsnd etctgagypq gkrmgrgapv epsreeplvs
      121 legsnsavtm elsepvveng evemaleesw ehskevseae pgggsssgdsg ppeesgqemm
      181 eekeeirksk svivpsgapk kehvnvvfig hvdagkstig gqimfltgmv dkrtlekyer
      241 eakeknretw ylswaldtnq eerdkgktve vgrayfeter khftildapg hksfvpnmig
      301 gasqadlavl visarkgefe tgfekggqtr ehamlaktag vkhlivlink mddptvnwsi
      361 eryeeckekl vpflkkvgfs pkkdihfmpc sgltganike qsdfcpwytg lpfipyldnl
      421 pnfnrsidgp irlpivdkyk dmgtvvlgkl esgsifkgqq lvmmpnkhnv evlgilsddt
      481 etdfvapgen lkirlkgiee eeilpgfilc dpsnlchsgr tfdvqiviie hksiicpgyn
      541 avlhihtcie eveitalisl vdkksgeksk trprfvkqdq vciarlrtag ticletfkdf
      601 pqmgrftlrd egktiaigkv lklvpekd
//
```


```
LOCUS       P62495                    437 aa            linear   PRI 01-OCT-2004
DEFINITION  Eukaryotic peptide chain release factor subunit 1 (eRF1)
            (Eukaryotic release factor 1) (TB3-1) (Cl1 protein).
ACCESSION   P62495
VERSION     P62495  GI:50402099
DBSOURCE    swissprot: locus ERF1_HUMAN, accession P62495;
            class: standard.
            extra accessions:P46055,created: Nov 1, 1995.
            sequence updated: Nov 1, 1995.
            annotation updated: Oct 1, 2004.
            xrefs: gi: 338686, gi: 338687, gi: 1491703, gi: 1491704, gi:
            1890299, gi: 1890300, gi: 5499720, gi: 5499721, gi: 1082824, pdb
            accession 1DT9
            xrefs (non-sequence databases): GenewHGNC:3477, MIM 600285,
            GO0005737, GO0003723, GO0003747, GO0006449, InterProIPR004403,
            InterProIPR005140, InterProIPR005141, InterProIPR005142,
            PfamPF03463, PfamPF03464, PfamPF03465, TIGRFAMsTIGR00108
KEYWORDS    3D-structure; Protein biosynthesis.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 437)
  AUTHORS   Grenett,H.E., Bounelis,P. and Fuller,G.M.
  TITLE     Identification of a human cDNA with high homology to yeast
            omnipotent suppressor 45
  JOURNAL   Gene 110 (2), 239-243 (1992)
  MEDLINE   92165066
   PUBMED   1537561
  REMARK    SEQUENCE FROM N.A.
REFERENCE   2  (residues 1 to 437)
  AUTHORS   Frolova,L., Le Goff,X., Rasmussen,H.H., Cheperegin,S., Drugeon,G.,
            Kress,M., Arman,I., Haenni,A.L., Celis,J.E., Philippe,M. et al.
  TITLE     A highly conserved eukaryotic protein family possessing properties
            of polypeptide chain release factor
  JOURNAL   Nature 372 (6507), 701-703 (1994)
  MEDLINE   95082951
   PUBMED   7990965
  REMARK    REVISIONS, AND FUNCTION.
REFERENCE   3  (residues 1 to 437)
  AUTHORS   Andjelkovic,N., Zolnierowicz,S., Van Hoof,C., Goris,J. and
            Hemmings,B.A.
  TITLE     The catalytic subunit of protein phosphatase 2A associates with the
            translation termination factor eRF1
  JOURNAL   EMBO J. 15 (24), 7156-7167 (1996)
  MEDLINE   97157506
   PUBMED   9003791
  REMARK    SEQUENCE FROM N.A.
            TISSUE=Brain
```

```
REFERENCE   4  (residues 1 to 437)
  AUTHORS   Guenet,L., Toutain,B., Guilleret,I., Chauvel,B., Deaven,L.L.,
            Longmire,J.L., Le Gall,J.Y., David,V. and Le Treut,A.
  TITLE     Human release factor eRF1: structural organisation of the unique
            functional gene on chromosome 5 and of the three processed
            pseudogenes
  JOURNAL   FEBS Lett. 454 (1-2), 131-136 (1999)
  MEDLINE   99339455
   PUBMED   10413110
  REMARK    SEQUENCE FROM N.A.
REFERENCE   5  (residues 1 to 437)
  AUTHORS   Song,H., Mugnier,P., Das,A.K., Webb,H.M., Evans,D.R., Tuite,M.F.,
            Hemmings,B.A. and Barford,D.
  TITLE     The crystal structure of human eukaryotic release factor
            eRF1--mechanism of stop codon recognition and peptidyl-tRNA
            hydrolysis
  JOURNAL   Cell 100 (3), 311-321 (2000)
  MEDLINE   20139983
   PUBMED   10676813
  REMARK    X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
COMMENT     On Jul 20, 2004 this sequence version replaced gi:1169547.
            ----------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ----------------------------------------------------------------.
            [FUNCTION] Directs the termination of nascent peptide synthesis
            (translation) in response to the termination codons UAA, UAG and
            UGA.
            [SUBUNIT] Heterodimer of two subunits, one of which binds GTP.
            [SUBCELLULAR LOCATION] Cytoplasmic.
            [SIMILARITY] Belongs to the eukaryotic release factor 1 family.
FEATURES             Location/Qualifiers
     source          1..437
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1..437
                     /gene="Name=ETF1"
                     /note="synonyms: Synonyms=ERF1,, RF1"
     Protein         1..437
                     /gene="Name=ETF1"
                     /product="Eukaryotic peptide chain release factor subunit
                     1"
     Region          7..9
                     /gene="Name=ETF1"
                     /region_name="Hydrogen bonded turn"
     Region          10..25
                     /gene="Name=ETF1"
                     /region_name="Helical region"
     Region          26
                     /gene="Name=ETF1"
                     /region_name="Hydrogen bonded turn"
     Region          34..39
                     /gene="Name=ETF1"
                     /region_name="Beta-strand region"
     Region          45..59
                     /gene="Name=ETF1"
                     /region_name="Helical region"
```

```
Region          60..61
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          65
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          66..82
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          83..84
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          90..91
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          93..101
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          103..105
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          107..114
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          120..121
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          124..128
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          134..139
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          145..150
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          158..162
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          163..164
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          165..170
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          188..197
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          198..203
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          204..208
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          209..213
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          225..228
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
```

```
Region          230..233
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          234..237
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          244..249
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          253..255
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          260..261
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          262..271
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          274..276
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          278..295
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          301..303
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          305..313
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          319..323
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          329
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          346
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          348..349
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          373
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          374..380
                /gene="Name=ETF1"
                /region_name="Helical region"
Region          381
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          383..386
                /gene="Name=ETF1"
                /region_name="Hydrogen bonded turn"
Region          389..392
                /gene="Name=ETF1"
                /region_name="Beta-strand region"
Region          397..404
                /gene="Name=ETF1"
                /region_name="Helical region"
```

```
     Region          405..408
                     /gene="Name=ETF1"
                     /region_name="Hydrogen bonded turn"
     Region          409..412
                     /gene="Name=ETF1"
                     /region_name="Beta-strand region"
ORIGIN
        1 maddpsaadr nveiwkikkl iksleaargn gtsmisliip pkdqisrvak mladefgtas
       61 niksrvnrls vlgaitsvqq rlklynkvpp nglvvycgti vteegkekkv nidfepfkpi
      121 ntslylcdnk fhtealtall sddskfgfiv idgsgalfgt lqgntrevlh kftvdlpkkh
      181 grggqsalrf arlrmekrhn yvrkvaetav qlfisgdkvn vaglvlagsa dfktelsqsd
      241 mfdqrlqskv lklvdisygg engfnqaiel stevlsnvkf iqekkligry fdeisqdtgk
      301 ycfgvedtlk alemgaveil ivyenldimr yvlhcqgtee ekilyltpeq ekdkshftdk
      361 etgqehelie smpllewfan nykkfgatle ivtdksqegs qfvkgfggig gilryrvdfq
      421 gmeyqggdde ffdlddy
//
```